



SEQUENCE LISTING

<110> SOLARI, ROBERTO CELESTE ERCOLE
CHAMPION, BRIAN ROBERT
WARD, GEORGE ALBERT

<120> CONJUGATE OF A TRANSPORT PROTEIN AND A PROTEIN FOR
MODULATION OF NOTCH SIGNALLING

<130> 674525-2007

<140> 10/720,896
<141> 2003-11-24

<150> PCT/GB02/02438
<151> 2002-05-24

<150> GB 0112818.0
<151> 2001-05-25

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<170> PatentIn Ver. 3.3

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<223> Description of Artificial Sequence: Synthetic PCR primer
for amplifying HES1 promoter from mouse genomic DNA

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<223> Description of Artificial Sequence: Synthetic PCR primer
for amplifying HES1 promoter from mouse genomic DNA

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<210> 3
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<223> Description of Artificial Sequence: Synthetic Adenovirus
major late promoter TATA-box motif with BglII and HindIII
cohesive ends

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<223> Description of Artificial Sequence: Synthetic Adenovirus
major late promoter TATA-box motif with BglII and HindIII
cohesive ends

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promoter tetramer with XhoI and BglII cohesive ends

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<223> Description of Artificial Sequence: Synthetic PCR
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human Notch1 cDNA

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<223> Description of Artificial Sequence: Synthetic Oligo
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from theNIC2202 fragment of human Notch1 cDNA

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Gly  Gly  Ala  Phe  Val  Gly  Pro  Arg  Cys  Gln  Asp  Pro  Asn  Pro  Cys  Leu
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Ser  Thr  Pro  Cys  Lys  Asn  Ala  Gly  Thr  Cys  His  Val  Val  Asp  Arg  Arg
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Gly  Val  Ala  Asp  Tyr  Ala  Cys  Ser  Cys  Ala  Leu  Gly  Phe  Ser  Gly  Pro
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Ser  Tyr  Ile  Cys  His  Cys  Pro  Pro  Ser  Phe  His  Gly  Pro  Thr  Cys  Arg
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          210          215          220

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His  Glu  Cys  Ala  Cys  Leu  Pro  Gly  Phe  Thr  Gly  Gln  Asn  Cys  Glu  Glu
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 1875 1880 1885

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 1925 1930 1935

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Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His
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Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val
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Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe
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Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser
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Cys	Ala	Pro	Ser	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	Arg	Gln	Thr	Gly	225	230	235
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Arg	Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cys	Tyr	Ser	Gln	705	710	715	720

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Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile	Ser	Gly	805	810	815
Tyr	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr	Thr	Gly	Lys	Asn	Cys	Gln	Thr	820	825	830
Val	Leu	Ala	Pro	Cys	Ser	Pro	Asn	Pro	Cys	Glu	Asn	Ala	Ala	Val	Cys	835	840	845
Lys	Glu	Ser	Pro	Asn	Phe	Glu	Ser	Tyr	Thr	Cys	Leu	Cys	Ala	Pro	Gly	850	855	860
Trp	Gln	Gly	Gln	Arg	Cys	Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile	Ser	Lys	865	870	875
Pro	Cys	Met	Asn	His	Gly	Leu	Cys	His	Asn	Thr	Gln	Gly	Ser	Tyr	Met	885	890	895
Cys	Glu	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Met	Asp	Cys	Glu	Glu	Asp	Ile	900	905	910
Asp	Asp	Cys	Leu	Ala	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Met	Asp	915	920	925
Gly	Val	Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Asp	930	935	940
Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn	945	950	955
Gly	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	Cys	Gln	965	970	975
Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	Cys	Thr	980	985	990
Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser	995	1000	1005
Phe	Ser	Cys	Leu	Cys	Pro	Val	Gly	Phe	Thr	Gly	Ser	Phe	Cys	Leu	His	1010	1015	1020

Glu Ile Asn Glu Cys Ser Ser His Pro Cys Leu Asn Glu Gly Thr Cys
 1025 1030 1035 1040
 Val Asp Gly Leu Gly Thr Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr
 1045 1050 1055
 Gly Lys Asn Cys Gln Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys
 1060 1065 1070
 Lys Asn Lys Gly Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu
 1075 1080 1085
 Cys Pro Ser Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser
 1090 1095 1100
 Cys Asp Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys
 1105 1110 1115 1120
 Gln His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys Gln
 1125 1130 1135
 Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu Asp Glu
 1140 1145 1150
 Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser Asp Phe Ile
 1155 1160 1165
 Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly Val Asn Cys
 1170 1175 1180
 Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn Gly Gly
 1185 1190 1195 1200
 Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro Pro Gly
 1205 1210 1215
 Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala Arg Gly
 1220 1225 1230
 Pro His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly Gly Tyr
 1235 1240 1245
 Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu Gly Asp
 1250 1255 1260
 Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser Leu Asp
 1265 1270 1275 1280
 Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe
 1285 1290 1295
 Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro
 1300 1305 1310
 Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly
 1315 1320 1325

Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser
 1330 1335 1340
 Ser Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr
 1345 1350 1355 1360
 Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu Ser
 1365 1370 1375
 Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His Pro Gln
 1380 1385 1390
 Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro Phe Ser Gly
 1395 1400 1405
 Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr Pro Pro Ala Thr
 1410 1415 1420
 Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val Cys Asp
 1425 1430 1435 1440
 Glu Ala Cys Asn Ser His Ala Cys Gln Trp Asp Gly Gly Asp Cys Ser
 1445 1450 1455
 Leu Thr Met Glu Asn Pro Trp Ala Asn Cys Ser Ser Pro Leu Pro Cys
 1460 1465 1470
 Trp Asp Tyr Ile Asn Asn Gln Cys Asp Glu Leu Cys Asn Thr Val Glu
 1475 1480 1485
 Cys Leu Phe Asp Asn Phe Glu Cys Gln Gly Asn Ser Lys Thr Cys Lys
 1490 1495 1500
 Tyr Asp Lys Tyr Cys Ala Asp His Phe Lys Asp Asn His Cys Asn Gln
 1505 1510 1515 1520
 Gly Cys Asn Ser Glu Glu Cys Gly Trp Asp Gly Leu Asp Cys Ala Ala
 1525 1530 1535
 Asp Gln Pro Glu Asn Leu Ala Glu Gly Thr Leu Val Ile Val Val Leu
 1540 1545 1550
 Met Pro Pro Glu Gln Leu Leu Gln Asp Ala Arg Ser Phe Leu Arg Ala
 1555 1560 1565
 Leu Gly Thr Leu Leu His Thr Asn Leu Arg Ile Lys Arg Asp Ser Gln
 1570 1575 1580
 Gly Glu Leu Met Val Tyr Pro Tyr Tyr Gly Glu Lys Ser Ala Ala Met
 1585 1590 1595 1600
 Lys Lys Gln Arg Met Thr Arg Arg Ser Leu Pro Gly Glu Gln Glu Gln
 1605 1610 1615
 Glu Val Ala Gly Ser Lys Val Phe Leu Glu Ile Asp Asn Arg Gln Cys
 1620 1625 1630

Val Gln Asp Ser Asp His Cys Phe Lys Asn Thr Asp Ala Ala Ala Ala
 1635 1640 1645
 Leu Leu Ala Ser His Ala Ile Gln Gly Thr Leu Ser Tyr Pro Leu Val
 1650 1655 1660
 Ser Val Val Ser Glu Ser Leu Thr Pro Glu Arg Thr Gln Leu Leu Tyr
 1665 1670 1675 1680
 Leu Leu Ala Val Ala Val Val Ile Ile Leu Phe Ile Ile Leu Leu Gly
 1685 1690 1695
 Val Ile Met Ala Lys Arg Lys Arg Lys His Gly Ser Leu Trp Leu Pro
 1700 1705 1710
 Glu Gly Phe Thr Leu Arg Arg Asp Ala Ser Asn His Lys Arg Arg Glu
 1715 1720 1725
 Pro Val Gly Gln Asp Ala Val Gly Leu Lys Asn Leu Ser Val Gln Val
 1730 1735 1740
 Ser Glu Ala Asn Leu Ile Gly Thr Gly Thr Ser Glu His Trp Val Asp
 1745 1750 1755 1760
 Asp Glu Gly Pro Gln Pro Lys Lys Val Lys Ala Glu Asp Glu Ala Leu
 1765 1770 1775
 Leu Ser Glu Glu Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr Gln Gln
 1780 1785 1790
 His Leu Glu Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala Leu Thr
 1795 1800 1805
 Pro Pro Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg
 1810 1815 1820
 Gly Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly
 1825 1830 1835 1840
 Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala
 1845 1850 1855
 Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln
 1860 1865 1870
 Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser
 1875 1880 1885
 Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn
 1890 1895 1900
 Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala
 1905 1910 1915 1920
 Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp
 1925 1930 1935

Leu Asp Ala Arg Met Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala
 1940 1945 1950
 Arg Leu Ala Val Glu Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala
 1955 1960 1965
 Asp Val Asn Ala Val Asp Asp His Gly Lys Ser Ala Leu His Trp Ala
 1970 1975 1980
 Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu Leu Lys Asn Gly
 1985 1990 1995 2000
 Ala Asn Arg Asp Met Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu
 2005 2010 2015
 Ala Ala Arg Glu Gly Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His
 2020 2025 2030
 Phe Ala Asn Arg Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp
 2035 2040 2045
 Val Ala Arg Asp Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu
 2050 2055 2060
 Tyr Asn Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu
 2065 2070 2075 2080
 Ser Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His
 2085 2090 2095
 Thr Pro Met Gly Lys Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met
 2100 2105 2110
 Pro Thr Ser Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly
 2115 2120 2125
 Ser Arg Arg Lys Lys Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser
 2130 2135 2140
 Ser Val Thr Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr
 2145 2150 2155 2160
 Val Ser Asp Thr Thr Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu
 2165 2170 2175
 Gln Ala Ser Pro Asn Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro
 2180 2185 2190
 Val His Ala Gln His Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln
 2195 2200 2205
 Pro Leu Ala His Gly Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu
 2210 2215 2220
 Leu Ser His His His Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser
 2225 2230 2235 2240

Leu Ser Arg Leu His Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg
 2245 2250 2255

Met Glu Val Asn Glu Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu
 2260 2265 2270

Ala Pro Ala Glu Gly Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro
 2275 2280 2285

Pro Glu Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile
 2290 2295 2300

Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly
 2305 2310 2315 2320

Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu
 2325 2330 2335

Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala
 2340 2345 2350

Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr
 2355 2360 2365

Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro
 2370 2375 2380

Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg
 2385 2390 2395 2400

Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr
 2405 2410 2415

Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser
 2420 2425 2430

Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala
 2435 2440 2445

Gly Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro Pro His
 2450 2455 2460

Asn Asn Met Gln Val Tyr Ala
 2465 2470

<210> 13

<211> 16

<212> PRT

<213> *Drosophila melanogaster*

<400> 13

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
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<210> 14
 <211> 16
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 <213> Artificial Sequence

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 Illustrative translocating peptide

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 <213> Artificial Sequence

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 Illustrative translocating peptide

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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 Illustrative translocating peptide fragment

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 <212> PRT
 <213> Human herpesvirus 1

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Asp Glu Tyr Glu Asp Leu Tyr Tyr Thr Pro Ser Ser Gly Met Ala Ser
 20 25 30

Pro Asp Ser Pro Pro Asp Thr Ser Arg Arg Gly Ala Leu Gln Thr Arg
 35 40 45

Ser Arg Gln Arg Gly Glu Val Arg Phe Val Gln Tyr Asp Glu Ser Asp
 50 55 60

Tyr Ala Leu Tyr Gly Gly Ser Ser Ser Glu Asp Asp Glu His Pro Glu
 65 70 75 80

Val Pro Arg Thr Arg Arg Pro Val Ser Gly Ala Val Leu Ser Gly Pro
 85 90 95

Gly Pro Ala Arg Ala Pro Pro Pro Pro Ala Gly Ser Gly Gly Ala Gly
 100 105 110

Arg Thr Pro Thr Thr Ala Pro Arg Ala Pro Arg Thr Gln Arg Val Ala
 115 120 125

Thr Lys Ala Pro Ala Ala Pro Ala Ala Glu Thr Thr Arg Gly Arg Lys
 130 135 140

Ser Ala Gln Pro Glu Ser Ala Ala Leu Pro Asp Ala Pro Ala Ser Thr
 145 150 155 160

Ala Pro Thr Arg Ser Lys Thr Pro Ala Gln Gly Leu Ala Arg Lys Leu
 165 170 175

His Phe Ser Thr Ala Pro Pro Asn Pro Asp Ala Pro Trp Thr Pro Arg
 180 185 190

Val Ala Gly Phe Asn Lys Arg Val Phe Cys Ala Ala Val Gly Arg Leu
 195 200 205

Ala Ala Met His Ala Arg Met Ala Ala Val Gln Leu Trp Asp Met Ser
 210 215 220

Arg Pro Arg Thr Asp Glu Asp Leu Asn Glu Leu Leu Gly Ile Thr Thr
 225 230 235 240

Ile Arg Val Thr Val Cys Glu Gly Lys Asn Leu Leu Gln Arg Ala Asn
 245 250 255

Glu Leu Val Asn Pro Asp Val Val Gln Asp Val Asp Ala Ala Thr Ala
 260 265 270

Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr Glu Arg Pro Arg Ala
 275 280 285

Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro Val Glu
 290 295 300